Anhydrous 1:1 proton-transfer compounds of isonipecotamide with picric acid and 3,5-dinitrosalicylic acid: 4-carbamoylpiperidinium 2,4,6-trinitrophenolate and two polymorphs of 4-carbamoylpiperidinium 2-carboxy-4,6-dinitrophenolate.

Graham Smith[a]* and Urs D. Wermuth[b]

[a]Faculty of Science and Technology, Queensland University of Technology, GPO Box 2434, Brisbane, Qld 4001, Australia, and [b]School of Biomolecular and Physical Sciences, Griffith University, Nathan, Qld 4111, Australia

Correspondence email: g.smith@qut.edu.au

The structures of the anhydrous 1:1 proton-transfer compounds of isonipecotamide (4-carbamoylpiperidine) with picric acid and 3,5-dinitrosalicylic acid, namely 4-carbamoylpiperidinium 2,4,6-trinitrophenolate, $C_6H_{13}N_2O_8^+$ $C_6H_2N_3O_7^-$ (I) and 4-carbamoylpiperidinium 2-carboxy-4,6-dinitrophenolate, $C_6H_{13}N_2O_8^+$ $C_7H_3N_2O_7^-$: two forms, the monoclinic α-polymorph (II) and the triclinic β-polymorph (III) have been determined at 200 K. All compounds form hydrogen-bonded structures, one-dimensional in (II), two-dimensional in (I) and three-dimensional in (III). In (I), the cations form centrosymmetric cyclic head-to-tail hydrogen-bonded homodimers [graph set $R^2_2(14)$] through lateral duplex piperidinium N—H···O_{amide} interactions. These dimers are extended into a two-dimensional network structure through further interactions with anion phenolate-O and nitro-O acceptors, including a direct symmetric piperidinium N—H···O_{phenol},O_{nitro} cation–anion association [graph set $R^2_1(6)$]. The monoclinic polymorph (II) has a similar $R^2_1(6)$ cation–anion hydrogen-bonding interaction to (I) but with an additional conjoint symmetrical $R^1_2(4)$ interaction as well as head-to-tail piperidinium N—H···O_{amide} O hydrogen bonds and amide N—H···$O_{carboxyl}$ hydrogen bonds, give a network structure which include large $R^3_4(20)$ rings. The hydrogen bonding in the triclinic polymorph (III) is markedly different from that of monoclinic (II). The asymmetric unit contains two independent cation–anion pairs which associate through cyclic piperidinium N–H···O,O'$_{carboxyl}$ interactions [graph set $R^2_1(4)$]. The cations also show the zig-zag head-to-tail piperidinium N—H···O_{amide}hydrogen-bonded chain substructures found in (II) but in addition feature amide N–H···O_{nitro} and $O_{phenolate}$ and amide N—H···O_{nitro} associations. As well there is a centrosymmetric double-amide N—H···$O_{carboxyl}$ bridged bis(cation–anion) ring system [graph set $R^2_4(8)$] in the three-dimensional framework. The structures reported here demonstrate the utility of the isonipecotamide cation as a synthon with previously unrecognized potential for structure assembly applications. Furthermore, the structures of the two polymorphic 3,5-dinitrosalicylic acid salts show an unusual dissimilarity in hydrogen-bonding characteristics, considering that both were obtained from identical solvent systems.

Comment

The structures of 4-piperidinecarboxylic acid (isonipecotic acid) (O'Neil, 2001) and its derivatives are uncommon in the crystallographic literature. Both anhydrous isonipecotic acid (Mora *et al.*, 2005) and its monohydrate (Delgado *et al.*, 2001) show the presence of piperidinium–carboxylate zwitterions while the structure of the hydrochloride is also known (Ma & Li, 2006); Adams *et al.*, 2007; Szafran *et al.*, 2007). However, neither the structure of its amide (isonipecotamide, INIPA) nor any of its derivatives had been reported, although the

structures of the acetate (Smith & Wermuth, 2010) and the bipyridine-4,4'-disulfonate (Smith *et al.*, 2010) are now known. . Picric acid has been used to produce stable crystalline Lewis base salts suitable for X-ray analysis and the number of picrate structures in the literature reflects this. Similarly, 3,5-dinitrosalicylic acid (DNSA) has proved to be a versatile synthon for crystal engineering usage (Kumar *et al.*, 1999) and a large number of structures of proton-transfer compounds with this acid have also been reported (Smith *et al.*, 2002, 2003, 2007). With these, the majority (*ca.* 70%) are phenolates rather than carboxylates, the H atom being *anti*-located on the carboxyl O within an intramolecular hydrogen bond.

We therefore carried out 1:1 stoichiometric reactions of isonipecotamide with a number of aromatic acids including picric acid and 3,5-dinitrosalicylic acid in 50% aqueous ethanol, with a view to obtaining crystals suitable for X-ray analysis, hence allowing description of the hydrogen-bonding present in these compounds. We obtained good crystals of the anhydrous picrate salt 4-carbamoylpiperidinium picrate $C_6H_{13}N_2O_8^+$ $C_6H_2N_3O_7^-$ (I) as well as two anhydrous polymorphic salts with DNSA, 4-carbamoylpiperidinium 2-carboxy-4,6-dinitrophenolate, $C_6H_{13}N_2O_8^+$ $C_7H_3N_2O_7^-$: the monoclinic (α) polymorph (II) and the triclinic (β) polymorph (III). The crystals of (II) were obtained after partial room temperature evaporation of solvent whereas with the identical parallel reaction in which the solution was taken to dryness, the second anhydrous triclinic polymorph (III) was obtained. The structures of (I)–(III) are described here, representing the first reported aromatic organic acid salts of the Lewis base isonipecotamide [excluding the biphenyl-4,4'-disulfonate salt (Smith *et al.*, 2010)]. It was of particular interest to determine what differences if any might be found in the hydrogen-bonding in the two polymorphic salts (II) and (III).

With salts (I)–(III) (Figs. 1–3), proton transfer occurs to the hetero-N of the piperidine ring and in each the resulting group, along with the amine substituent group are subsequently involved in hydrogen-bonding interactions (Tables 1–3). All three salts are phenolates and form hydrogen-bonded structures, one-dimensional in (II), two-dimensional in (I) and three-dimensional in (III). A feature of hydrogen-bonding motifs in (II) and (III) is the presence of homomolecular head-to-tail piperidinium N—H···O_{amide} interactions giving infinite zig-zag chain structures.

In (I), the two piperidinium H donors give three hydrogen-bonding interactions. One of the hydrogen atoms gives a symmetric cyclic $R^2_1(6)$ association (Etter *et al.*, 1990) with phenolate O and nitro O-acceptors of the anion (Fig. 1). The second proton forms a hydrogen bond with an amide O-acceptor giving a centrosymmetric cyclic head-to-tail homodimer [graph set $R^2_2(14)$] (Table 1, Fig. 4). This ring is conjoint with an piperidine N—H···O_{amide} cyclic $R^2_4(8)$ association and the previously mentioned $R^2_1(6)$ association. These rings are linked by other amide N–H···O_{nitro} interactions into a two-dimensional network structure which lies in the (O 1 1) plane with the picrate ring systems layering down the *b* axis of the unit cell. The *ortho*-related nitro substituent groups of the picrate anion are significantly rotated out of the benzene plane [torsion angles C1–C2–N2–O22, 134.13 (16)°; C5–C6–N6–O62, -157.57 (16)°], comparing with 176.78 (14)° for C3–C4–N4–O42 for the *para*-nitro group.

In the monoclinic α-polymorph of the 3,5-dinitrosalicylic acid salt (II), a cyclic $R^2_1(6)$ proximal piperidinium N—H···O_{phenol},O_{nitro} cation–anion association similar to that in (I) is present (Fig. 2). This is also similar to the

association found in a number of DNSA proton-transfer compounds (Smith *et al.*, 2007) but in (II), with an additional conjoint symmetrical $R^2_1(4)$ piperidinium N–H···O,O' interaction (Fig. 2). Head-to-tail piperidinium N—H···O_{amide} hydrogen bonds (Table 2) give ribbon structures which extend along the *b* cell direction and enclose $R^3_4(20)$ ring systems (Fig. 5). The short intramolecular hydrogen bond which is characteristic of the DNSA anion is found in (II) as well as in the triclinic polymorph (III). In both structures the *anti*-related proton is located on the carboxyl group rather than on the phenolic O, but this is the majority case with the DNSA anions in the known structures of the proton-transfer salts of this acid (Smith *et al.*, 2002, 2003, 2007).

The triclinic modification (the β-polymorph) of the isonipecotamide-DNSA compound (III) has two INPA cations (*A*, *B*) as well as two anions (*C*, *D*) in the asymmetric unit (Fig. 3). Although there is not any major difference in the amide side chain conformations of the two independent cations in (III) [as indicated by the torsion angle C3–C4–C41–N41 [93.6 (2)° (*A*) cf. 86.5 (2)° (*B*)], these differ significantly from that found in (II) [122.29 (16)°]. With the DNSA anions the differences are less obvious. As expected because of the presence of the intramolecular hydrogen bond, the carboxylic acid group is essentially coplanar with the benzene ring in all three anions [torsion angle C2–C1–C11–O11: -179.15 (16)° (II); -178.18 (18)° (III*C*); -179.09 (16)° (III*D*)]. Both nitro groups in the two polymorphs are slightly rotated out of the plane [torsion angles C2–C3–N3–O32: 165.64 (17)° (II); -170.75 (16)° (III*C*); -177.65 (15)° (III*D*); and C4–C5–N5–O52: -166.78 (16)° (II); -175.98 (17)° (III*C*); -170.94 (18)° (III*D*)]. However, the hydrogen-bonding differences between (II) and (III) are very significant (Table 3). There is an absence of the proximal piperidinium N–H···$O_{phenolate}$,O_{nitro} interaction with either of the DNSA anions. Instead, one of the cations (*B*) gives an N—H···O,$O'_{carboxyl}$ interaction with a *D* anion [graph set $R^2_1(4)$], the other (*A*) acting as a bridge between cation *B* amide-O and anion nitro-O acceptors. The anions also form the zig-zag head-to-tail piperidinium N—H···O_{amide} bridged chain hydrogen-bonded chain substructures also found in (II) (Fig. 6). In addition the hydrogen bonding in the overall three-dimensional framework structure features a centrosymmetric duplex amide H–N–H bridged bis(cation–anion) $R^2_4(8)$ ring system (Fig. 6).

The structures reported here demonstrate the utility of the isonipecotamide cation as a synthon with previously unrecognized potential for structure assembly applications. Furthermore, the structures of the two polymorphic 3,5-dinitrosalicylic acid salts (II) and (III) show unusually diverse hydrogen-bonding characteristics with only slight molecular conformational differences. In the absence of any additive induced effects during crystallization, the observed polymorphism can be seen as an artefact of solvent gradient effects, considering that the parallel crystallizations occurred from identical ethanol–water solvent mixtures.

Experimental

The title compounds were synthesized by heating together for 10 minutes under reflux, 1 mmol quantities of 4-carbamoylpiperidine (isonipecotamide) and 2,4,6-trinitrophenol (picric acid) [for (I)] or 3,5-dinitrosalicylic acid [for (II) and (III)] in 50 mL of 50% ethanol–water. After concentration to *ca.* 30 mL, partial room temperature evaporation [(I) and (III)] or evaporation to dryness (II) of the hot-filtered solutions gave yellow prisms of (I) (m.p. 452 K) or yellow plates of (II) and (III) (m.p. 475 K).

(I)

Crystal data

$C_6H_{13}N_2O\cdot C_6H_2N_3O_7$	V = 1519.2 (3) Å^3
M_r = 357.29	Z = 4
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation, λ = 0.71073 Å
a = 13.4426 (11) Å	μ = 0.13 mm^{-1}
b = 13.7495 (13) Å	T = 200 K
c = 8.3662 (15) Å	0.25 × 0.20 × 0.15 mm
β = 100.752 (13)°	

Data collection

Oxford Diffraction Gemini-S Ultra CCD-detector diffractometer	2994 independent reflections
Absorption correction: Multi-scan *CrysAlis PRO* (Oxford Diffraction, 2009)	2279 reflections with $I > 2\sigma(I)$
T_{min} = 0.950, T_{max} = 0.981	R_{int} = 0.034
10181 measured reflections	

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.036	0 restraints
$wR(F^2)$ = 0.107	H atoms treated by a mixture of independent and constrained refinement
S = 0.93	$\Delta\rho_{max}$ = 0.26 e Å^{-3}
3422 reflections	$\Delta\rho_{min}$ = −0.28 e Å^{-3}
238 parameters	

Table 1

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N1*A*—H11*A*···O1	0.934 (18)	1.901 (17)	2.7545 (19)	150.8 (15)
N1*A*—H11*A*···O62	0.934 (18)	2.227 (17)	2.859 (2)	124.3 (13)
N1*A*—H12*A*···O41*A*^{i}	0.912 (18)	2.012 (18)	2.8932 (19)	162.0 (16)
N41*A*—H43*A*···O41*A*^{ii}	0.866 (17)	2.029 (17)	2.894 (2)	177 (2)
N41*A*—H44*A*···O1^{iii}	0.910 (19)	2.316 (19)	3.072 (2)	140.3 (15)
N41*A*—H44*A*···O22^{iv}	0.910 (19)	2.437 (19)	3.017 (2)	121.8 (14)

Symmetry codes: (i) −*x*, −*y*+1, −*z*+1; (ii) *x*, −*y*+1/2, *z*−1/2; (iii) −*x*, *y*−1/2, −*z*+1/2; (iv) −*x*, −*y*+1, −*z*.

(II)

Crystal data

$C_7H_3N_2O_7\cdot C_6H_{13}N_2O$	V = 1547.1 (3) Å^3
M_r = 356.30	Z = 4
Monoclinic, $P2_1/n$	Mo $K\alpha$ radiation, λ = 0.71073 Å
a = 11.7131 (12) Å	μ = 0.13 mm^{-1}
b = 12.6450 (11) Å	T = 200 K

c = 11.8521 (14) Å
β = 118.196 (14)°
0.40 × 0.40 × 0.20 mm

Data collection

Oxford Diffraction Gemini-S Ultra CCD-detector diffractometer
Absorption correction: Multi-scan *CrysAlis PRO* (Oxford Diffraction, 2009)
T_{min} = 0.93, T_{max} = 0.98
19733 measured reflections
3048 independent reflections
2456 reflections with $I > 2\sigma(I)$
R_{int} = 0.033

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.039
$wR(F^2)$ = 0.098
S = 1.06
3048 reflections
242 parameters
0 restraints
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.31 e Å^{-3}
$\Delta\rho_{min}$ = −0.24 e Å^{-3}

Table 2

Hydrogen-bond geometry (Å, º)

D—H···A	D—H	H···A	D···A	D—H···A
N1A—H11A···O2	0.86 (2)	1.98 (2)	2.817 (2)	164 (2)
N1A—H11A···O31	0.86 (2)	2.43 (2)	2.835 (3)	109.7 (17)
N1A—H12A···O31	0.93 (2)	2.43 (2)	2.835 (3)	106.1 (15)
N1A—H12A···O41A^{i}	0.93 (2)	1.844 (19)	2.6964 (19)	151 (2)
N41A—H41A···O11^{i}	0.88 (2)	2.19 (2)	3.053 (2)	168 (2)
O12—H12···O2	1.01	1.52	2.4829 (17)	157

Symmetry code: (i) $-x+3/2$, $y+1/2$, $-z+1/2$.

(III)

Crystal data

$C_7H_3N_2O_7 \cdot C_6H_{13}N_2O$
M_r = 356.30
Triclinic, $P\overline{1}$
a = 6.4628 (4) Å
b = 10.2375 (5) Å
c = 23.8964 (12) Å
α = 98.644 (4)°
β = 96.905 (5)°
γ = 100.753 (5)°
V = 1517.65 (15) Å^3
Z = 4
Mo $K\alpha$ radiation, λ = 0.71073 Å
μ = 0.13 mm^{-1}
T = 200 K
0.40 × 0.30 × 0.18 mm

Data collection

Oxford Diffraction Gemini S Ultra CCD-detector diffractometer
Absorption correction: Multi-scan CrysAlis PRO (Oxford Diffraction, 2009)
5940 independent reflections
4477 reflections with I > 2σ(I)

T_{min} = 0.96, T_{max} = 0.98	R_{int} = 0.026
19052 measured reflections	

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.039	0 restraints
$wR(F^2)$ = 0.095	H atoms treated by a mixture of independent and constrained refinement
S = 0.82	$\Delta\rho_{max}$ = 0.23 e Å^{-3}
5940 reflections	$\Delta\rho_{min}$ = −0.23 e Å^{-3}
475 parameters	

Table 3

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N1*A*—H11*A*···O32*C*^{i}	0.91 (2)	2.113 (19)	2.980 (2)	160.1 (17)
N1*A*—H12*A*···O41*B*	0.93 (2)	1.86 (2)	2.759 (2)	159.7 (19)
N1*B*—H11*B*···O41*A*^{ii}	0.92 (2)	1.91 (2)	2.757 (2)	153 (2)
N1*B*—H12*B*···O11*D*	0.97 (3)	2.09 (3)	3.039 (2)	167 (2)
N1*B*—H12*B*···O12*D*	0.97 (3)	2.26 (2)	2.980 (2)	131 (2)
N41*A*—H41*A*···O2*D*^{iii}	0.86 (2)	2.18 (2)	2.954 (2)	148.8 (19)
N41*A*—H42*A*···O51*D*^{iv}	0.91 (2)	2.18 (2)	2.999 (2)	149.0 (18)
N41*B*—H41*B*···O11*C*^{v}	0.90 (2)	2.34 (2)	3.176 (2)	154.9 (18)
N41*B*—H41*B*···O12*C*^{v}	0.90 (2)	2.58 (2)	3.388 (2)	149.5 (18)
N41*B*—H42*B*···O11*C*	0.89 (2)	2.09 (2)	2.950 (2)	164.3 (19)
O12*C*—H12*C*···O2*C*	1.12	1.38	2.460 (2)	157
O12*D*—H12*D*···O2*D*	1.10	1.37	2.4422 (18)	163

Symmetry codes: (i) −*x*+2, −*y*+1, −*z*+1; (ii) *x*−1, *y*−1, *z*; (iii) −*x*, −*y*, −*z*; (iv) −*x*, −*y*+1, −*z*; (v) −*x*, −*y*, −*z*+1.

Hydrogen atoms involved in hydrogen-bonding interactions were located by difference methods and with the exception of the carboxylic H in both (II) and (III) which were allowed to ride, their positional and isotropic displacement parameters were refined. The other H-atoms were included in the refinements at calculated positions [C–H(aliphatic) = 0.99, 1.00 Å and C–H(aromatic) = 0.95 Å) while using a riding model approximation, with U_{iso}(H) = 1.2U_{eq}(C).

Data collection: *CrysAlis PRO* (Oxford Diffraction, 2009) for (I); *CrysAlis PRO* for (II), (III). For all compounds, cell refinement: *CrysAlis PRO*. Data reduction: *CrysAlis PRO* for (II), (III). Program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008) for (I); *SIR92* (Altomare, 1994) for (II), (III). Program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008) for (I); *SHELXL97* (Sheldrick, 2008) within *WinGX* (Farrugia, 1999) for (II), (III). Molecular graphics: *PLATON* (Spek, 2009) for (I), (II); *PLATON*(Spek, 2009) for (III). For all compounds, software used to prepare material for publication: *PLATON*.

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Figure 1

Fig. 1. Molecular configuration and atom naming scheme for the isonipecotamide cation and the picrate anion in (I). Displacement ellipsoids are drawn at the 50% probability level. Intermolecular hydrogen bonds are shown as dashed lines.

Figure 2

Fig. 2. Molecular configuration and atom naming scheme for the isonipecotamide cation and the DNSA anion in (II). Displacement ellipsoids are drawn at the 50% probability level. Inter- and intramolecular hydrogen bonds and short molecular contacts are shown as dashed lines.

Figure 3

Fig. 3. Molecular configuration and atom naming scheme for the two isonipecotamide cations (*A* and *B*) and the two DNSA anions (*C* and *D*) in the asymmetric unit of (III). Displacement ellipsoids are drawn at the 50% probability level. Inter-species hydrogen bonds are shown as dashed lines

Figure 4

Fig. 4. The two-dimensional hydrogen-bonded network structure of (I) extending across the (0 1 0) plane of the unit cell, showing hydrogen-bonding associations as dashed lines. Non-associative H atoms are omitted. For symmetry codes, see Table 1.

Figure 5

Fig. 5. The one-dimensional hydrogen-bonded ribbon structure of (II) extending along the *b* cell direction, showing hydrogen-bonding associations and short inter-ion associations as dashed lines. Non-associative H atoms are omitted. For symmetry codes, see Table 2.

Figure 6

Fig. 6. The three-dimensional hydrogen-bonded framework structure of (III) in a perspective view of the unit cell, showing hydrogen-bonding associations as dashed lines. Non-associative H atoms are omitted. For symmetry codes, see Table 3.